

Figure 1: Nucleotide Sequence of TbF14  
Sheet 1 of 4

FEATURES	Location/Qualifiers
misc_feature	5072..5095
	/note="His tag coding region"
misc_feature	5096..7315
	/note="MtB81 coding region"
misc_feature	7316..8594
	/note="Mo2 coding region"

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Figure 1: Nucleotide Sequence of TbF14  
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Figure 1: Nucleotide Sequence of TbF14  
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Figure 1: Nucleotide Sequence of TbF14  
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Figure 2: Nucleotide sequence of TbF15  
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FEATURES	Location/Qualifiers
misc_feature	5072..5095
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misc_feature	5096..5293
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misc_feature	5294..6346
	/note="38kD coding region"
misc_feature	6347..6643
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Figure 2: Nucleotide sequence of TbF15  
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Figure 2: Nucleotide sequence of TbF15  
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GCGTAGAGGATCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGG  
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GATTTCCAGCGCTGAGATGAAGACCGATGCCGCTACCCTCGCGCAGGAGGCAGGTAATTTTCGAGCG  
GATCTCCGGCGACCTGAAAACCCAGATCGACCAGGTGGAGTGCACGGCAGGTTTCGTTGCAGGGCCA  
GTGGCGCGGCGCGCGGGGACGGCCGCCAGGCCCGGTGGTGCGCTTCCAAGAAGCAGCCAATAA  
GCAGAAGCAGGAATCGACGAGATCTCGACGAATATTCGTCAGGCCGGCGTCCAATACTCGAGGGC  
CGACGAGGAGCAGCAGCAGGCGCTGTCTCGCAAATGGGCTTTACTCAGTCGCAGACCGTGACGGT  
GGATCAGCAAGAGATTTTGAACAGGGCCAACGAGGTGGAGGCCCGATGGCGGACCCACCGACTGA  
TGTCCCCATCACACCGTGCGAACTCACGGCGGCTAAAAACGCCGCCCAACAGCTGGTATTGTCCGC  
CGACAACATGCGGGAATACCTGGCGGCCGGTGCCAAAGAGCGGCAGCGTCTGGCGACCTCGCTGCG  
CAACGCGGCCAAGGCGTATGGCGAGGTTGATGAGGAGGCTGCGACCGCGCTGGACAACGACGGCGA  
AGGAATGTGCAGGCAGAATCGGCCGGGGCGTCGGAGGGGACAGTTCGGCCGAACCTAACCGATAC  
GCCGAGGGTGGCCACGGCCGGTGAACCCAACCTTCATGGATCTCAAAGAAGCGGCAAGGAAGCTCGA  
AACGGGCGACCAAGGCGCATCGCTCGCGCACTTTGCGGATGGGTGGAACACTTTCAACCTGACGCT  
GCAAGGCGACGTCAAGCGGTTCCGGGGGTTTGACAACCTGGGAAGGCGATGCGGCTACCGCTTGCGA  
GGCTTCGCTCGATCAACAACGGCAATGGATACTCCACATGGCCAAATTGAGCGCTGCGATGGCCAA  
GCAGGCTCAATATGTGCGCGCAGCTGCACGTGTGGGCTAGGCGGGAACATCCGACTTATGAAGACAT  
AGTCGGGCTCGAACGGCTTTACGCGGAAAACCTTCGGCCCGCGACCAAATTCTCCCGGTGTACGC  
GGAGTATCAGCAGAGGTCGGAGAAGGTGCTGACCGAATAACAACAAGGCAGCCCTGGAACCGGT  
AAACCCGCCGAAGCCTCCCCCGCCATCAAGATCGACCCGCCCGCCCTCCGCAAGAGCAGGGATT  
GATCCCTGGCTTCTGATGCCGCCGTCTGACGGCTCCGGTGTGACTCCCGGTACCGGGATGCCAGC  
CGCACCGATGGTTCCGCTACCGGATCGCCGGGTGGTGGCCTCCCGGCTGACACGGCGGCGCAGCT  
GACGTGCGCTGGGCGGGAAGCCGCGAGCGCTGTGCGGCGACGTGGCGGTCAAAGCGGCATCGCTCGG  
TGGCGGTGGAGGCGGCGGGGTGCCGTCGGCGCCGTTGGGATCCGCGATCGGGGGCGCCGAATCGGT

09688672-11111111

Figure 2: Nucleotide sequence of TbF15  
Sheet 4 of 4

GCGGCCCCGCTGGCGCTGGTGACATTGCCGGCTTAGGCCAGGGAAGGGCCGGCGGGCGCCGCGCT  
GGGCGGCGGTGGCATGGGAATGCCGATGGGTGCCGCGCATCAGGGACAAGGGGGCGCCAAGTCCAA  
GGGTTCTCAGCAGGAAGACGAGGCGCTCTACACCGAGGATCGGGCATGGACCGAGGCCGTCATTGG  
TAACCGTCGGCGCCAGGACAGTAAGGAGTCGAAGTGAATTCTGCAGATATCCATCACACTGGCGGC  
CGCTCGAGCACCACCACCACCACCTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGT  
TGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGG  
GTTTTTGTGCTGAAAGGAGGAAGTATATCCGGAT

09688672-101000



Figure 3: Amino Acid Sequence of TbF14

MQHHHHHTDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDE  
LQAQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSQVDAEITTTAGPQLVVPVLNAR  
FALNAANARWGSLYDALYGTVDVIPETDGAKEGPTYNKVRGDKVIAYARKFLDDSVPLSSGSFGDAT  
GFTVQDQQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEILIDPESQVGTTRAGV  
KDVI LESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDGTAFRLVLRDRNYTAP  
GGGQFTLPGRSLMFVRNVGHLMTNDIAIVDTDGSEVFEGIMDALFTGLIAIHGLKASDVNGPLINSR  
TGSIIYIVKPKMHGPAEVAFTCELSRVEDVLGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVF  
INTGFLDRTGDEIHTSMEAGPMVRKGTMKSPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTTEL  
MADMVETKIAQPRAGASTAWVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKEL  
AWAPDEIREVDNNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISQLLANWLRHGV  
TSADVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSI AFLAAQELILSGAQQPNGYTEPILHRRRR  
EFKARAAEKPA PSDRAGDDAARVQKYGGSSVADAERIRRV AERIVATKKQGNDVVVVVSAMGDTTD  
DLLDLAQQVCPAPPPRELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKII  
DVTGRLQTAL EGRVVLVAGFQGVSDTKDVTTLGRGGSDDTAVAMAAALGADVCEIYTDVDGIF  
SADPRIVRNARKLDTVTFEEMLEMAACGAKVLMRLCVEYARRHNPVHVRSSYSRPGTVVVGSIK  
DVP MEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRVARRRRQHRHGAAERLQGRGRQDRHHL  
HLLPQTSGPPPWKWTRSETRSASTQLLYDDHIGKVSLIGAGMRSHPGVTATFCEALAAVGVNIEL  
ISTSEDQSRCCAATPNWTRPWSRCMKRSGSAATRRPRCTRGRDGRWACQ..

000101-2798960

Figure 4: Amino Acid Sequence of TbF15

MGHHHHHHVIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITRYIKLEVSF  
KMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWGPAFHRYPNVTI  
TAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISAQQVNYNLPGVSEHLKLNG  
KVLAAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQDPEGWGKSPGF  
GTTVDFFPAVPGALGENGNNGMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNSSGNFLLPDAQ  
SIQAAAAGFASKTPANQAISMIDGPAPDGYPIINYEYAIVNNRQKDAATAQTLQAFHLHWAITDGNK  
ASFLDQVHFQPLPPAVVKLSDALIATISSAEMKTDAAATLAQEAGNFERISGDLKTQIDQVESTAGS  
LQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQALSSQMGFTQSQ  
TVTVDQQEILNRANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNMREYLAAGAKERQRLA  
TSLRNAAKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDSSAELTDTPRVATAGEPNFMDLKEAA  
RKLETGDQGASLAHFADGWNTFNLTQGDVKRFRGFDNWEQDAATAACEASLDQQRQWILHMAKLSA  
AMAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPSARDQILPVYAEYQQRSEKVLTEYNNKAA  
LEPVNPPKPPPAIKIDPPPPPPQEQGLIPGFLMPPSDGSGVTPGTGMPAAPMPVPTGSPGGGLPADT  
AAQLTSAGREAAALSGDVAVKAASLGGGGGGGVPSAPLGSAGGAESVRPAGAGDIAGLGQGRAGG  
GAALGGGGMGMPMGAAHQGGGAKSKGSQQEDEALYTEDRAWTEAVIGNRRRQDSKESK.

09588672-101000

Figure 5

	Status	TbF15	TbF6
5004	TB	0.926	1.045
7004	TB	0.928	1.184
9004	TB	1.102	1.365
11004	TB	0.856	1.629
15004	TB	2.035	2.099
17004	TB	2.893	2.867
18004	TB	0.477	0.414
21004	TB	1.062	1.635
23004	TB	0.429	0.501
26004	TB	0.299	0.392
27004	TB	0.244	0.207
28004	TB	2.236	2.04
30004	TB	2.058	1.508
32004	TB	2.324	1.927
33004	TB	1.600	1.578
34004	TB	1.059	1.136
36004	TB	0.546	1.105
37004	TB	1.446	1.989
39004	TB	2.021	2.782
41004	TB	0.511	0.652
43004	TB	0.855	0.483
44004	TB	0.731	0.66
53004	TB	1.100	0.317
FD8-24	Control	0.183	0.314
FD8-25	Control	0.061	0.063
FD8-26	Control	0.066	0.142
FD8-27	Control	0.021	0.115
FD8-28	Control	0.053	0.289
FD8-29	Control	0.114	0.238
FD8-30	Control	0.105	0.146
FD8-31	Control	0.101	0.237
FD8-33	Control	0.080	0.071
FD8-34	Control	0.140	0.117
FD8-35	Control	0.088	0.072
FD8-36	Control	0.081	0.089
FD8-37	Control	0.057	0.06
FD8-38	Control	0.104	0.111
FD8-39	Control	0.221	0.241
FD8-40	Control	0.257	0.265
FD8-41	Control	0.056	0.093
FD8-42	Control	0.184	0.273
FD8-43	Control	0.126	0.126
FD8-44	Control	0.193	0.092
FD8-45	Control	0.058	0.057
FD8-46	Control	0.183	0.23
FD8-48	Control	0.062	0.085
FD8-49	Control	0.134	0.247
Mean		0.113	0.157
SD		0.061	0.086
Mean +3SD		0.298	0.414
Sensitivity		22/23	20/23

CAGGCATGAGCAGAGCGTTTCATCATCGATCCAAAGATGAGTGGCATTGACGGCTTGACAGCTTCTGGGGAATGGAATACCCAAAGGGGGTATCCT  
GTCCGTACTCGTCTCGCAAGTAGTAGCTAGGTTGCTAGTCACGGTAAGTCCGAACATGCTGGAAGACCCCTAACCTTATGGGTGGTTCCTCCCATAGGA 100

## HTCC-1 FL

M S R A F I I D P T I S A I O G L Y D L L G I G I P N Q G G I L  
TTACTCCTCACTAGAGTACTTCGAAAAAGCCCTGGAGGAGCTGGCAGCAGCGTTTCGGGGTGAATGGCTGGTTAGGTTGGGCGCGGACAAATACGCCGGC  
AATGAGGAGTGATCTCATGAAGCTTTTTTCGGGACCTCTCGACCGTCTGCGCAAGGCCCACTACCGACCAATCCAAAGCCGGCGCTGTTTATGCGGGCG 200

## HTCC-1 FL

Y S S L E Y F E K A L E E L A A A F P G D G W L G S A A D K Y A G  
AAAAACCGCAACCACGTGAATTTTTTCCAGGAAGTGGCAGACCTCGATCGTCAGCTCATCAGCCTGATCCACGACCAGGCCAACCGGGTCCAGACGACCC  
TTTTTGGCGTTGGTGCACTTAAAAAGGTCTTTGACCGTCTGGAGCTAGCAGTCGAGTAGTCGGACTAGGTGCTGGTCCGGTTGCGCCAGGTCTGCTGGG 300

## HTCC-1 FL

X N R N H V N F F Q E L A D L D R D L I S L I H D Q A N A V Q T T  
GCGACATCCTGGAGGGCGCCAAGAAAGGTCTCGAGTTGCTGGCGCCGGTGGCTGTGGACCTGACCTACATCCCGGTCGTCGGGCACGCCCTATCGGCCGC  
CGCTGTAGGACCTCCCGCGGTTCTTTCCAGAGCTCAAGCACGCGGGCCACCGACACCTGGACTGGATGTAGGGCCAGCAGCCCGTGGGGATAGCCGGCG 400

## HTCC-1 FL

R D I L E G A K K G L E F V R P V A V D L T Y I P V V G H A L S A A  
CTTCAGGGCGCGTTTTTGGCGGGCGCGATGGCCGTAGTGGCGGGCGCGCTTGCCCTACTTGGTCGTGAAAACGCTGATCAACCGGACTCAACTCCTCAAA  
GAAGGTCCGCGGCAAAACGCGCCCGCTACCGGCATACCCGCGCGCGGAACGGATGAACCAGCACTTTTGGCACTAGTTGCGCTGAGTTGAGGAGTTT 500

## HTCC-1 FL

F Q A P F C A G A M A V V G G A L A Y L V V K T L I N A T Q L L K  
TTGCTTGCCAAATTGGCGGAGTTGGTGGCGGCCGCCATTGGCGACATCATTTCCGATGTGGCGGACATCATCAAGGGCACCCCTCGGAGAAGTGTGGGAGT  
AACGAACGGTTTAAACCGCTCAACCAGCGCGGGCGGTAACGCCCTGTAGTAAAGCCTACACCGCCTGTAGTAGTTCCCGTGGGAGCCTCTTCACACCCCTCA 600

## HTCC-1 FL

L L A K L A E L V A A A I A D I I S O V A D I I K G T L G E V W E  
TCATCACAACCGCTCAACGGCTGAAAGAGCTTTGGGACAAGCTCACGGGGTGGGTGACCGGACTGTTCTCTCGAGGGTGGTCAACCTGGAGTCTCTT  
AGTAGTGTGTCGCGAGTTGCCGGACTTTCTCGAAACCTGTTGAGTGCCCCACCCACTGGCCTGACAAGAGAGCTCCACCCAGCTTGGACCTCAGGAA 700

## HTCC-1 FL

F I T N A L N G L K E L W D K L T G W V T G L F S R G W S N L E S F  
CTTTGCGGGCGTCCCGGCTTGACCGGCGGACCGCGGCTTGTGCAAGTGACTGGCTTGTTGGGTGCGGCCGGTCTGTCCGCATCGTCGGGCTTGGCT  
GAAACGCGCGCAGGGGCGGAAGTGGCCGCGCTGGTGGCCGAACAGCGTTCACTGACCGAACAAGCCACGCGCGCCAGACAGGCGTAGCAGCCCGAACC GA 800

## HTCC-1 FL

F A G V P G L T G A T S G L S Q V T G L F G A A G L S A S S G L A

Fig. 6

sheet 1 of 2

CACGCGGATAGCCTGGCGAGCTCAGCCAGCTTCTCCCTGGCGGCAATTGGGGGCGGGTCCGGTTTTGGGGGCGCGAGCCTGGCTCAGGTCCATG  
GTGCGCCTATCGGACCGCTCGAGTCGGTCCGAACGGGCGGACCGCGCTAACCCCGCCAGGCCAAAACCCCGCAACGGCTCGGACCGAGTCCAGGTAC

900

HTCC-1 FL

H A D S L A S S A S L P A L A G I G G G S G F G G L P S L A Q V H

CCGCTCAACTCGGCAGGCGCTACGACCCCGAGCTGATGGCCCGGTCCGCGCCGCTGCCGAGCAGGTCCGCGGCGAGTCCGAGCTGGTCTCCGCGCAGGG  
GGCGGAGTTGAGCGGTCCGCGATGCCGGGGCTCGACTACCGGGCCAGCGCGCGGACGGCTCGTCCAGCCGCCCGTCAGCGTCCAGCAGAGGCGCGTCCC

1000

HTCC-1 FL

A A S T R Q A L R P R A Q G P V G A A A E Q V G G Q S Q L V S A Q G

TTCCCAAGGTATGGGCGGACCCGTAGGCATGGGCGGCATGCACCCCTCTTCGGGGGCGTCGAAAGGGACGACGACGAAGAAGTACTCGGAAGGCGCGCG  
AAGGGTTCCATACCCCGCTGGGCATCCGTACCCGCGGTACGTGGGGAGAAGCCCCGCGAGCTTTCCTGCTGCTGCTTCTTCATGAGCCTTCCGCGCCGC

1100

HTCC-1 FL

S Q G M G G P V G M G G M H P S S G A S K G T T T K K Y S E G A A

GCGGGCACTGAAGACGCCGAGCGCGCGCCAGTCGAAGCTGACGCGGGCGGTGGGCAAAAGGTGCTGGTACGAAACGTCGCTAACGGCATGGCGAGCCAA  
CGCCCGTGACTTCTGCGGCTCGCGCGCGGTACGCTTCGACTGCGCCCGCCACCCGTTTTCCACGACCATGCTTTGCAGCAGATTGCCGTACCGCTCGGTT

1200

HTCC-1 FL

A G T E D A E R A P V E A D A G G G Q K V L V R N V V

0968672-111077

FIG. 6

Sheet 2 of 2

Monday, July 26, 1999 10:49 AM  
TCC1(1:232) Map.mpd (1 > 726) Site and Seq  
Enzymes: 212 of 515 enzymes (Filtered)  
Settings: Linear, Certain Sites Only, Standard Genetic Code

HTCC-1 (1-222)

Page 1

ATGCATCACCATCACCATCACA TGACGAGAGCGTTCATCATGATCCAACGATCAGTGCCATTGACGGCTTGTACGAGCTTCTGGGGATTGGAATACCCA  
TACGTAGTGGTAGTGGTAGTGTACTGCTCTGCAAGTAGTAGCTAGGTTGCTAGTCAAGGTAACGCGCAACATGCTGGAAGACCCCTAACCTTATGGGT  
M H H H H H H M S R A F I I O P T I S A I O G L Y D L L G I G I P  
ACCAAGGGGTATCCTTTACTCCTCACTAGAGTACTTGGAAAAGCCCTGGAGGAGCTGGCAGCAGCGTTTCCGGGTGATCGCTGGTTAGGTTCCGGCCGC  
TGGTTCCTCCCATAGGAAATGAGGAGTGTCTCATGAAGCTTTTTCGGGACCTCCTCGACCGTGTGCGCAAGGGCCACTACCGACCAATCCAAGCCGGCG  
N O G G I L Y S S L E Y F E K A L E E L A A A F P G D G W L G S A A  
GGACAAATACGCCGGCAAAAACCGCAACGCTGAATTTTTTCCAGGAACGGCAGACCTCGATCGTCAGTCTATCAGCGTGATCCAGGACAGGCCAAC  
CCTGTTTATGCGGCCGTTTTTGGCGTTGGTGCACTTAAAAAAGGTCTTGACCGTCTGAGGCTAGCAGTCCAGTAGTCCGACTAGGTGCTGGTCCGGTTG  
O K Y A G K N R N H V N F F Q E L A O L O R Q L I S L I H O O A N  
GCGGTCCAGACGACCCGCGACATCCTGGAGGGCGCAAGAAGGTCTCGAGTTCTGCGCCCGGTGGCTGTGGACCTGACCTACATCCCGGTGCTCGGGC  
CGCCAGGTCTGCTGGGCGCTGTAGGACCTCCCGCGGTTCTTTCCAGAGCTCAAGCACGCGGGCCACCGACACCTGGACTGGATGTAGGGCCAGCAGCCCG  
A V Q T T R D I L E G A K K G L E F V R P V A V D L T Y I P V V G  
ACGCCCTATCGGCCGCTTCCAGGCGCGTTTTGCGGGGCGCGATGGCCGTAGTGGGCGGGCGGCTTGCCCTACTTGGTGGTGA AAAACGCTGATCAACGC  
TGCGGGATAGCCGGCGGAAGGTCCGCGGCAAAAACGCGCCCGCGCTACCGGCATCACCCGCGCGCGGAACGGATGAACAGCACTTTTGGGACTAGTTGGC  
H A L S A A F Q A P F C A G A M A V V G G A L A Y L V V K T L I N A  
GACTCAACTCCTCAAATTGCTTGCCAAATTGGCGGAGTTGGTGGCGGCGCCATTGCGGACATCATTTCCGATGTGGCGGACATCATCAAGGGCATCCTC  
CTGAGTTGAGGAGTTTAACGAACGGTTTAAACCGCTCAACCGAGCGCGCGGTAACGCTGTAGTAAAGCCTACACCGCTGTAGTAGTTCCCGTAGGAG  
T O L L K L L A K L A E L V A A A I A D I I S O V A O L I K G I L  
GGAGAAGTGTGGGAGTTCATCACAACGCGCTCAACGGCTGAAAGAGCTTTGGGACAAGCTCACGGGTGGGTGACCGGACTGTTCTCTCGAGGGTGGT  
CCTCTTACACCCCTCAAGTAGTGTGCGCGAGTTGCGGAGCTTTCTCGAAACCTGTTTCGAGTGCCCCACCCACTGGCCTGACAAGAGAGCTCCCA  
G E V W E F I T N A L N G L K E L W D K L T G W V T G L F S R G W  
CGAACCTGGAGTCTTCTAAGAATTC  
GCTTGGACCTCAGGAAGATTCTTAAG  
S N L E S F E F

Fig. 7a

Monday, July 25, 1999 10:50 AM

HTCC1(134-392) Map.mpd (1 &gt; 361) Site and S

Enzymes: 212 of 515 enzymes (Filtered)

Settings: Linear, Certain Sites Standard Genetic Code

ATGCATCACCATCACCATCACGATGTGGCGGACATCATCAAGGGCATCCTCGGAGAAGTGTGGGAGTTTCATCACAACGGGCTCAACGGGCTGAAAGAGC  
100  
TACGTAGTGGTAGTGGTAGTGCTACACCGCGCTGTAGTAGTTCCGGTAGGAGCCCTCTTCACACCCCTCAAGTAGTGTTCGGCGAGTTGCCGGACTTTCTCG  
M H H H H H H D V A O I I K G I L G E V W E F I T N A L N G L K E  
TTTGGGACAAGCTCACGGGGTGGGTGACCGGACTGTTCTCTCGAGGGTGGTGAACCTGGAGTCCCTTCTTTGGCGCGTCCCGGGCTTGACCGGGCGGAC  
200  
AAACCCCTGTTTCGAGTCCCGCCACCCACTGGGCTGACAAGAGAGCTCCACCCAGCTTGGACCTCAGGAAGAAACGGCGCGAGGGCCGAACCTGGCCCGCTG  
L W D K L T G W V T G L F S R G W S N L E S F F A G V P G L T G A T  
CAGCGGCTTGTGCAAGTGACTGGCTTGTTCGGTGGCGCGGCTGTGTCGGCATCGTGGGCTTGGCTCAGCGGATAGCCTGGCGAGCTCAGCCAGCTTG  
300  
GTGCGCGAACAGCGTTCACTGACCGAACAAGCCACGCGCGCCAGACAGGCGTAGCAGCCCGAACCAGAGTGCCTATCGGACCGCTCGAGTCCGTCGAAC  
S G L S Q V T G L F G A A G L S A S S G L A H A O S L A S S A S L  
CCCCCCTGGCGGGCATTGGGGGCGGGTCCGGTTTTGGGGGCTTGGCGAGCCTGGCTCAGGTCCATGCCGCCCTCAACTCGGCAGGCGCTACGGCCCCGAG  
400  
GGGCGGGACCGCGGTAACCCCCGCGCCAGGCCAAAACCCCGGAACGGCTCGGACCGAGTCCAGGTACGGCGGAGTTGAGCGTCCGCGATGCCGGGGCTC  
P A L A G I G G G S G F G G L P S L A Q V H A A S T R Q A L R P R  
CTGATGGCCCCGGTCCGGCGCGCTGCCGAGCAGTCCGGCGGCGAGTCCGAGCTGGTCTCCGCGCAGGGTTCCCAAGGTATGGCGGACCCGTAGGCATGGG  
500  
GACTACCGGGCCAGCCGCGCGGCGACGGCTCGTCCAGCCGCCCCGTACGCGTCGACCAGAGGCGCGTCCCAAGGGTTCCATACCCGCTGGGCATCCGTACCC  
A O G P V G A A A E Q V G G Q S Q L V S A Q G S Q G M G G P V G M G  
CGGCATGCACCCCTCTTCGGGGGCGTCGAAAGGGACGACGACGAAGAAGTACTCGGAAGGCGCGCGCGGGGCACTGAAGACGCCGAGCGCGGCCAGTC  
600  
GCCGTACGTGGGGAGAAGCCCCCGCAGCTTTCCCTGCTGCTGCTTCTTCATGAGCCTTCCGCGCGCGCGCGCGTGACTTCTGCGGCTCGCGCGCGGTCAG  
G M H P S S G A S K G T T T K K Y S E G A A A G T E D A E R A P V  
GAAGCTGACGCGGGCGGTGGGCAAAAGGTGCTGGTACGAAACGTCGCTAACGGCGAATTC  
661  
CTTCGACTGCGCCCGCCACCCGTTTTCCACGACCATGCTTTGCAGCAGATTGCCGCTTAAG  
E A D A G G G Q K V L V R N V V R R I

FIG. 7b

Monday, July 26, 1999 10:48 AM  
TCC1(1-129) Map.MPD (1 > 411) Site and sequence  
Enzymes: All 515 enzymes (No  
Settings: Circular, Certain Sites, Standard Genetic Code

H1C-1 (1-129)

Page 1


ATGCATCACCATCACCATCACATGAGCAGAGCGTTCATCATCGATCCAACGATCAGTGCCATTGACGGCTTGACGACCTTCTGGGGATTGG 92  
TACGTAGTGGTAGTGGTAGTGTACTCGTCTCGCAAGTAGTAGCTAGGTGCTAGTCACGGTAACTGCGGAACATGCTGGAAGACCCCTAACC  
M H H H H H H M S R A F I I O P T I S A I O G L Y D L L G I G  
AATACCCAACCAAGGGGGTATCCTTTACTCCTCACTAGAGTACTTCGAAAAAGCCCTGGAGGAGCTGGCAGCAGCGTTTCCGGGTGATGGCT 134  
TTATCGGTTGGTTCCCCCATAGGAAATGAGGAGTGATCTCATGAAGCTTTTTCCGGACCTCCTCGACCGTCTGCGCAAAGGCCCACTACCGA  
I P N O G G I L Y S S L E Y F E K A L E E L A A A F P G D G  
GGTTAGGTTCCGGCCGCGGACAAATACGCCGGCAAAAAACCGCAACCCAGTGAATTTTTTCCAGGAACCTGGCAGACCTCGATCGTCAGCTCATC 276  
CCAATCCAAGCCGGCGCCTGTTTATGCGGCCGTTTTTGGCGTTGGTGCACCTAAAAAAGGTCTCTGACCGTCTGAGCTAGCAGTCGAGTAG  
W L G S A A O K Y A G K N R N H V N F F Q E L A O L O R Q L I  
AGCCTGATCCACGACCAGGCCAACGCGGTCCAGACGACCCGCGACATCCTGGAGGGCGCCAAGAAAAGGTCTCGAGTTCGTGCGCCCGGTGGC 368  
TCGGAAGTAGGTGCTGGTCCGGTTGCGCCAGGTCTGCTGGGCGCTGTAGGACCTCCCGCGGTCTTTTCCAGAGCTCAAGCACGCGGGCCACCG  
S L I H D Q A N A V Q T T R O I L E G A K K G L E F V R P V A  
TGTGGACCTGACCTACATCCCGGTGCTCGGGCACGCCCTATAG 411  
ACACCTGGACTGGATGTAGGGCCAGCAGCCCGTGCGGGATATC  
V O L T Y I P V V G H A L

FIG. 7c

09688672-101000



2/27/91 TCC1 type (1 > 1629) Site and Sequence

Enzymes: All 515 enzymes are from   
 Genetics: Linear. Certain Sites Only. Standard Genetic Code

enzymes: Linear. Certain Sites On Standard Genetic Code

bindings: CATATGCATCACCATCACCATCACACGGGCGCGGTCCGATAACTTCCAGCTGTGCCAGGGTGGGCAGGGATTCCGCATTCCGATCCAGCAGGCGATGGCGA 100

GTATACGTAGTGGTAGTGGTAGTGTGCCGGCGCAGGCTATTGAAGGTCGACAGGGTCCCAACCGTCCCTAAGCGGTAAGGCTAGCCCGTCCCGCTACCGCT


11 Ra12

Met / HIS TAG  
H M H H H H H T A A S D N F Q L S Q G G Q G F A I P I G Q A M A  
TCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCACCGGTCATATCGGGCCTACCGGCTTCCTCGGCTTGGGTGTTGTGACAAACAACGGCAACGGCGC  
AGCGCCCGGTCTAGGCTAGCCCAACCCCAAGTGGGTGGCAAGTATAGCCCGGATGGCGGAAGGAGCCGAACCCACAACAGCTGTTGTTGCCGTTGCCGCGC

I A G Q I R S G G G S P T V H I G P T A F L G L G V V O N N G N G. A  
 ACCGAGTCCAACGCGTGGTCGGGAGCGCTCGGGCGGCAAGTCTCGGCATCTCCACCGGGCAGCTGATCACC GCGGTGCGACGGCGCTCCGATCAACTCGGCC  
 TGCTCAGGTTGCGCACCCAGCCCTCGCGAGGGCGCGCTTCAGAGCGGTAGAGGTGGCGCGCTGCACTAGTGGCGCCAGCTGCCGCGAGGCTAGTTGAGCCG 300  
 Ra12

R V Q R V V G S A P A A S L G I S T G D V I T A V D G A P I N S A  
 ACCGCGATGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCATCTGGGTGACCTGGCAAACCAAGTCGGGGCGGCACGCGTACAGGGAACGTGACAT  
 TGGCGCTACCGCTGCGCGAAATTGCCCGTAGTAGGGCCACTGCAGTAGAGCCACTGGACCGTTTGGTTTCAGCCCGCGGTGCGCATGTCCCTTGCACTGTA

T A M A D A L N G H H P G D V I S V T W Q T K S G G T R T G N V T  
TGGCCGAGGGACCCCCGGCGGAATTCTAGTAGCTACGTAGAGGTTCAATGAGCAGAGCGTTTCATCATCGATCCAACGATCAGTGCCATTGACGGCTTGTACGA=500  
ACCGGCTCCCTGGGGGCCGGCTTAAGGATCATGGATCTCCAAGTTACTCGTCTCGCAAGTAGTAGCTAGGTTGCTAGTCACGGTAACTGCCGAACATGCT


  
 L A E G P P A E F L V P R G S M S R A F I I D P T I S A I D G L Y D
   
 C C T T C T G G G G A T T G G A A T A C C C A A C C A A G G G G G T A T C C T T T A C T C C T C A C T A G A G T A C T T C G A A A A A G C C C T G G A G G A G C T G G C A G C A G C G T T T C C G G G T
   
 G G A A G A C C C T A A C C T T A T G G G T T G G T T C C C C C A T A G G A A T G A G G A G T G A T C T C A T G A A G C T T T T T C G G G A C C T C C T C G A C C G T C G T C G C A A A G G C C C A
   
 hTCC1

L L G I G I P N G G G I L Y S S L E Y F E K A L E E L A A A F P G  
 GATGGCTGGTTAGGTTGCGCCGCGGACAAATACGCGGCAAAAACCGCAACCACGTGAATTTTTTCCAGGAACCTGGCAGACCTCGATCGTCAGCTCATCA  
 CTACCGACCAATCCAAGCGGGCGCCTGTTTATGCGGCCGTTTTGGCGTTGGTGCACTTAAAAAGGTCCTTGACCGTCTGGAGCTAGCAGTCGAGTAGT

O G W L G S A A D K Y A G K N R N H V N F F G E L A O L O R O L I  
 GCCTGATCCACGACCAGGCCAACGCGGTCCAGACGACCCGCGACATCCTGGAGGGCGCCAAGAAAGGTCTCGAGTTCGTGCGCCCGGTGGCTGTGGACCT  
 CGGACTAGGTGCTGGTCCGGTTGCGCCAGGTCTGCTGGGCGCTGTAGGACCTCCGCGGTTCTTTCCAGAGCTCAAGCACGCGGGCCACCGACACCTGGA  
 hTCC1

S L I H D Q A N A V Q T T R D I L E G A K K G L E F V R P V A V O L  
 GACCTACATCCCGGTCGTCGGGCACGCCCTATCGGCCGCTTCCAGGCGCGTTTTGCGCGGGCGCGATGGCCGTAGTGGGCGGCGCGCTTGCCCTACTTG  
 CTGGATGTAGGGCCAGCAGCCCGTGCGGGATAGCCGGCGGAAGGTCCGCGGCAAAACGCGCCCGCGCTACCGGCATCACCGCCGCGCGGAACGGATGAAC

T Y I P V V G H A L S A A F Q A P F C A G A M A V V G G A L A Y L

FIG. 8

Sheet 1 of 2

1TCGTTGAAAACGCTGATCAACGCGACTCAACTC...AATTGCTTGCCAAATTGGCGGAGTTGGTGGGGGGGGC...CGGACATCATTTCCGATGTGG 1000  
CAGCACTTTTGGCACTAGTTGGCGGTGAGTTGAGGAGTTTAAACGAACGGTTTAAACCGCTCAACCCAGCGCGGGCGTAAACGCTGTAGTAAAGCCTACACC  
hTCC1  
V V K T L I N A T G L L K L L A K L A E L V A A A I A D I I S D V  
CGGACATCATCAAGGGCATECTCGGAGAAGTGTGGGAGTTTCATCACAACCGGCTCAACGGCTGAAAGAGCTTTGGGACAAGCTCACGGGGTGGGTGAC 1100  
GCCTGTAGTAGTTCCCGTAGGAGCCTCTTCACACCCCTCAAGTAGTGTTTGCGCGAGTTGCGCGACTTTCTCGAAACCCCTGTTCGAGTGCCCCACCCACTG  
hTCC1  
A D I I K G I L G E V W E F I T N A L N G L K E L W D K L T G W V T  
CGGACTGTCTCTCGAGGGTGGTGAACCTGGAGTCTCTTTTGGCGGCTCCCGGGCTTGACCGGGCGGACCCAGCGGCTTGTGCAAGTGACTGGCTTG 1200  
GCCTGACAAGAGAGCTCCACCCAGCTTGGACCTCAGGAAGAAGACGCCCGCAGGGGCGGAACCTGCGCGCTGGTGGCGGAACAGCGTTCACTGACCGAAC  
hTCC1  
G L F S R G W S N L E S F F A G V P G L T G A T S G L S D V T G L  
TTCGGTGGCGCGGCTGTGTCGGCATCGTGGGCTTGGCTCAGCGGATAGCCTGGCGAGCTCAGCCAGCTTGGCGGCCCTGGCGGGCATTGGGGGCGGGT 1300  
AAGCCACGCCCGGCGAGACAGGCGTAGCAGCCGAACCGAGTGGCGCTATCGGACCGCTCGAGTCGGTCTGAACGGGCGGGACCGGCCGTAAACCCCGGCCA  
hTCC1  
F G A A G L S A S S G L A H A D S L A S S A S L P A L A G I G G G  
CCGGTTTTTGGGGGCTTGGCGAGCCTGGCTCAGGTCCATGCCSCCTCAACTCGGCAGGCGCTACGGCCCGAGCTGATGGCCCGGTGGCGCGGCTGCCGA 1400  
GGCCAAAACCCCGAACGGCTCGGACCGAGTCCAGGTACGGCGGAGTTGAGCCGTCCGCGATGCCGGGGCTCGACTACCGGGCCAGCCGCGCGGACGGCT  
hTCC1  
S G F G G L P S L A Q V H A A S T R Q A L R P R A D G P V G A A A E  
GCAGGTGGCGGGCAGTGGCAGCTGGTCTCCGCGCAGGTTCCCAAGGTATGGGCGGACCCGTAGGCATGGGCGGCATGCACCCCTCTTCGGGGGCGTGG 1500  
CGTCCAGCCGCCCGTCCAGCTCGACCGAGGGCGGTCCCAAGGTTCCATACCCGCTGGGCATCCGTACCCGCGGTACGTGGGGAGAAGCCCCGCGAGC  
hTCC1  
Q V G G Q S Q L V S A Q G S Q G M G G P V G M G G M H P S S G A S  
AAAGGGACGACGACGAAGAAGTACTCGGAAGGCGCGGCGGGCGGCGACTGAAGACGCCGAGCGCGGCCAGTCGAAGCTGACGCGGGCGGTGGGCAAAAGG 1600  
TTTCCCTGTCTGCTTCTTCATGAGCCTTCCGCGCGCGCGCGCGTGACTTCTGCGGCTCGCGCGCGGTGAGCTTCGACTGCGCCCGCCACCCGTTTTC  
hTCC1  
K G T T T K K Y S E G A A A G T E O A E R A P V E A D A G G G Q K  
TGCTGGTACGAAACGTCGTTCTAAGAATTC 1629  
ACGACCATGCTTTGCAGCAGATTCTTAAG  
hTCC1 EcoRI  
V L V R N V V E F

FIG. 8

Sheet 2 of 2

Thursday, July 22, 1999 1:35 PM

TCC1(-TD.1).mpd (1 > 1225) Site and Sequen

Enzymes: 2 of 515 enzymes (Filtered)

Settings: Linear, Certain Sites On Standard Genetic Code

HTCC-1 (T7.1)

Page 1

CATATGCATCACCATCACCATCACATGAGCAGAGCGTTTCATCGATCGCAACGATCAGTGGCATTGACGGCTTGTACGACCTTCGCGGATTGGAATAC  
GTATACGTAGTGGTAGTGGTAGTGTACTCGTCTCGCAAGTAGTAGGTAGGTTCCTAGTCACGGTAACTCGCGAACATGCTGGAAGACCCCTAACCTTATG 100  
Met / HIS TAG HTCC1  
H M H H H H H M S R A F I I O P T I S A I O G L Y O L L G I G I  
CCAACCAAGGGGGTATCCCTTTACTCCTCACTAGAGTACTTCGAAAAAGCCCTGGAGGAGCTGGCAGCAGCGTTTCGCGGTGATGGCTGGTTAGGTTCGGC 200  
GGTTGGTTCCCCCATAGGAAATGAGGAGTGATCTCATGAAGCTTTTCGCGGACCTCCTCGACCGTCTGTCGCAAGGCCCACTACCGACCAATCCAAGCCG  
HTCC1  
P N O G G I L Y S S L E Y F E K A L E E L A A A F P G O G W L G S A  
CGCGGACAAATACGCCGGCAAAAACCGCAACCACGTGAATTTTTTCAGGAACCTGGCAGACCTCGATCGTCAGCTCATCAGCCTGATCCACGACCAGGCC 300  
GCGCCTGTTTATGCGGCGGTTTTGGCGTTGGTGCACTTAAAAAAGTGCTTTGACCGTCTGGAGCTAGCAGTCTGAGTCTGGACTAGGTGCTGGTCCGG  
HTCC1  
A O K Y A G K N R N H V N F F O E L A O L O R O L I S L I H O O A  
AACGCGGTCCAGACGACCCGCGACATCCTGGAGGGCGGCAAGAAAGGTCTCGAGTTCTGCGCCCGGTGGCTGTGGACCTGACCTACATCCCGGTGCTCG 400  
TTGCGCCAGGTCTGCTGGGCGCTGTAGGACCTCCCGCGTTCTTTTCAGAGCTCAAGCAGCGGGGCCACCGACACCTGGACTGGATGTAGGGCCAGCAGC  
HTCC1  
N A V Q T T R O I L E G A K K G L E F V R P V A V O L T Y I P V V  
GGCAGCGCCTATCGGCCGCTTCCAGGCGCGTTTTGCGCGGCGCGATGGCGCTAGTGGGCGGCGCGCTTAAGCTTGCCCTACTTGGTCTGAAAAAGCT 500  
CCGTGCGGGATAGCGGCGGAAGGTCCGCGGCAAAACGCGCGCGCTACCGGCATCAGCGCGCGCGAATTGGAACGGATGAACAGCACTTTTGGGA  
HTCC1 Hind3 DELETED  
G H A L S A A F O A P F C A G A M A V V G G A L K L A Y L V V K T L  
GATCAACGCGAAGCTTACTCAACTCCTCAAATTGCTTGCCAAATTGGCGGAGTTGGTGGCGGCGGCCATTGGCGGACATCATTTGGATGTGGCGGACATC 600  
CTAGTTGCGCTTCGAATGAGTTGAGGAGTTTAACGAACGGTTTAACCGCTCAACCAGCGCGGCGGTAACGCTGTAGTAAAGCTACACCGCTGTAG  
DELETED Hind3 HTCC1  
I N A K L T O L L K L L A X L A E L V A A A I A D I I S O V A O I  
ATCAAGGGCATCCTCGGAGAAGTGTGGGAGTTCATCACAACCGCTCAACGGCTGAAAGAGCTTTGGGACAAGCTCACGGGTGGGTGACCGGACTGT 700  
TAGTTCCCGTAGGAGCCTCTTCACACCTCAAGTAGTGTTCGCGGAGTTGCCGGACTTTCTCGAAACCTGTTTCGAGTGCCCCACCCACTGGCTGACA  
HTCC1  
I K G I L G E V W E F I T N A L N G L K E L W O K L T G W V T G L  
TCTCTGAGGGTGGTGAACCTGGAGTCTCTTTTGGCGGCTCCCGGCTTGACCGGCGCGACCAGCGGCTTGTGCAAGTGAAGTGGCTTGTTCGGTGC 800  
AGAGAGCTCCACCAAGCTTGGACCTCAGGAAGAAACGCGCAGGGGCGGAACCTGGCGCGCTGGTGGCGAAGACGGTTCACTGACCGAACAAGCCAGC  
HTCC1  
F S R G W S N L E S F F A G V P G L T G A T S G L S O V T G L F G A  
GGCGGTCTGTCCGCATCGTCGGCTTGGCTCACGCGGATAGCCTGGCGAGCTCAGCCAGCTTGCCCGCCTGGCGGCAATTGGGGCGGGTCCGGTTTT 900  
CCGGCCAGACAGGCGTAGCAGCCGAACCGAGTGCCTATCGGACCGCTCGAGTGGTGAACGGGCGGGACCGGCGTAACCCCGCCAGGCCAAAA  
HTCC1  
A G L S A S S G L A H A O S L A S S A S L P A L A G I G G G S G F

FIG. 9a

Sheet 1 of 2

3GGGGCTTGGCGAGCCTGGGTCAGGTCCATGCCCAACTGGGCAGGCGCTACGGCCCCGAGCTGATGGCCGGCGCGCTGCCGAGCAGGTGG  
1000  
CCCCCGAACGGCTCGGACCGAGTCCAGGTACGGCGGAGTTGAGCCGTCCGCGATGCCGGGGCTCGACTACCGGGCTAGCCCGCGGACGGCTCGTCCAGC  
hTCC1  
G G L P S L A Q V H A A S T R Q A L R P R A D G P V G A A A E Q V  
GGGGGCAGTGGCAGCTGGTCTCCGCGCAGGGTTCCCAAGGTATGGGCGGACCCGTAGGCATGGGCGGCATGCACCCCTCTTCGGGGGCGTCGAAAGGGAC  
1100  
CGCCCGTCAGCGTCGACCGAGAGGCGCGTCCCAAGGGTTCCATACCCGCTGGGCATCGGTACCCGCGCTACGTGGGGAGAAGCCCCCGCAGCTTTCCCTG  
hTCC1  
G G Q S G L V S A Q G S G G M G G P V G M G G M H P S S G A S K G T  
GACGACGAAGAAGTACTCGGAAGGCGCGGGCGGGCGGCACTGAAGACGCCGAGCGCGCGCAGTCGAAGCTGACGCGGGCGGTGGGCAAAAGGTGCTGGTA  
1200  
CTGCTGCTTCTTCATGAGCCTTCGCGCGCGCGCGCGTGACTTCTGCGGCTCGCGCGCGGTCAGCTTCGACTGCGCGCGCGCACCCGTTTTCCACGACCAT  
hTCC1  
T T K K Y S E G A A A G T E D A E R A P V E A D A G G G Q X V L V  
CGAAACGTCGTCTAACGGCGAATTC  
1225  
GCTTTGCAGCAGATTGCCGCTTAAG  
hTCC1 EcoRI  
R N V V . R R I

FIG. 9a

Sheet 2 of 2

09688672-111000

Friday, February 19, 1999 2:28 PM  
 HCC1 peptides.seq Map (1 > 1179) Site and Sequence  
 Enzymes: All 470 enzymes (No Filter)  
 Settings: Linear, Certain Sites Only, Standard Genetic Code

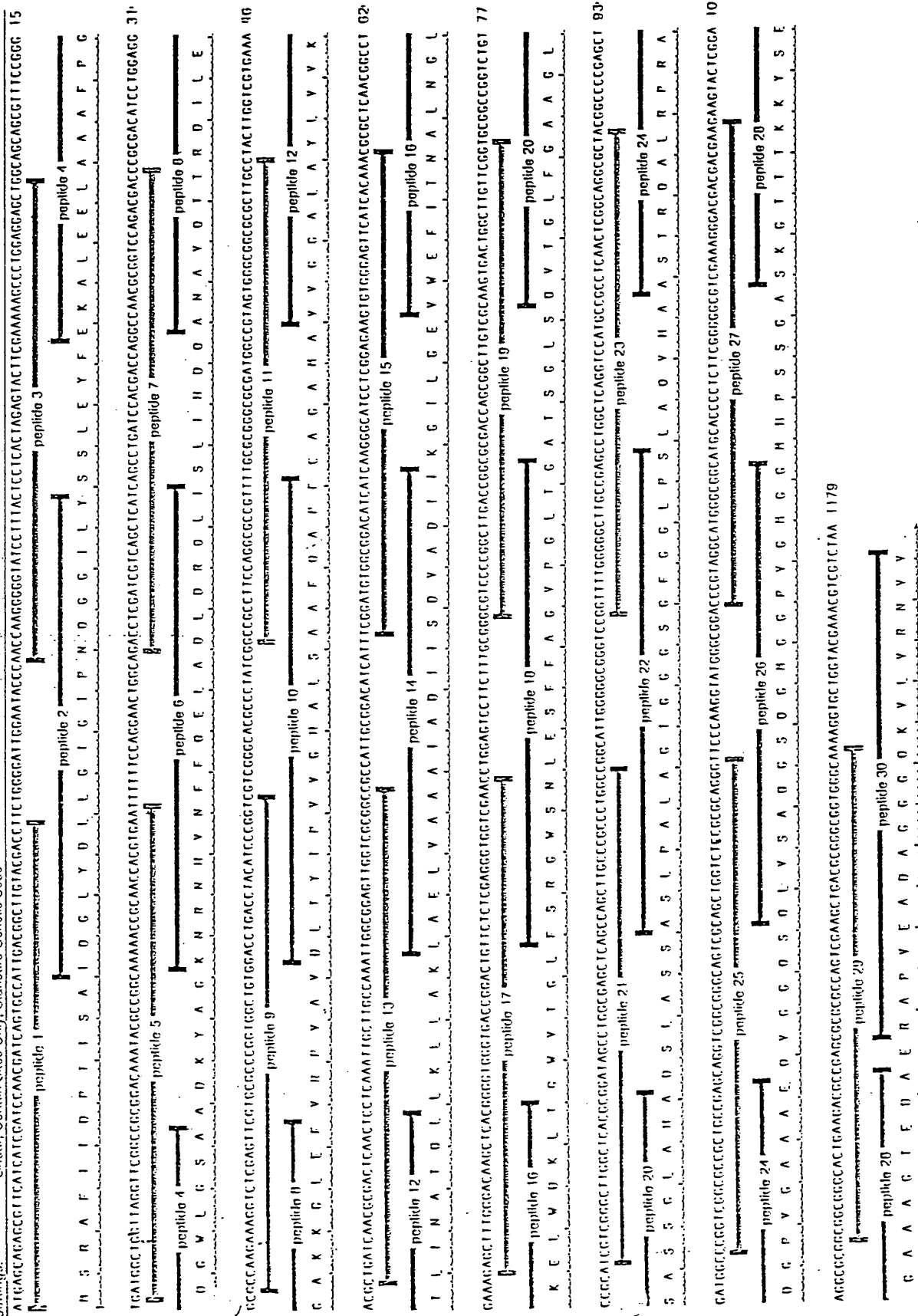


Fig. 96

# T Cell Epitope Mapping of HTCC-1

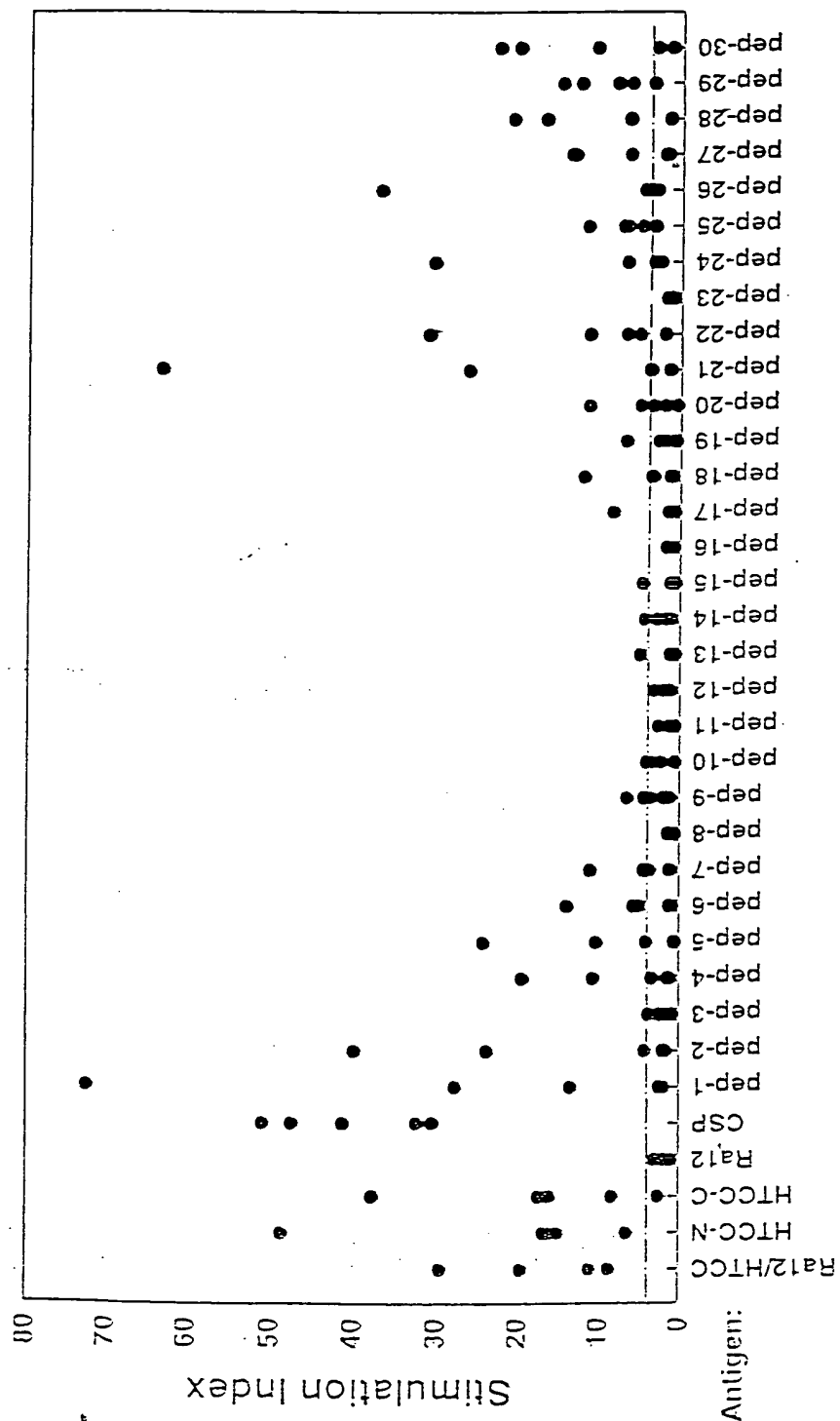


FIG. 9c

CATATGCATCACCATCACCATCACATGAGCAGAGGCTTCATCATCGATCCAAACGATCAGTGGCAATGAGGCTTGACGACCTTCTGGGGA  
GTATACGTAGTGGTAGTGGTAGTGTACTCGTCTCGCAAGTAGTAGCTAGGTTGCTAGTCACGGTAACGCGCAACATGCTGGAAGACCCCT

91

hTCC1

H M H H H H H H M S R A F I I O P T I S A I O G L Y O L L G

TTGGAATACCCAACCAAGGGGGTATCCTTTACTCCTCACTAGAGTACTTCGAAAAAGCCCTGGAGGAGCTGGCAGCAGCGTTTCCGGGTGA  
AACCTTATGGGTTGGTTCCCCCATAGGAAATGAGGAGTGATCTCATGAAGCTTTTTCGGGACCTCCTCGACCGTCGTCGCAAAGGCCCACT

182

hTCC1

I G I P N O G G I L Y S S L E Y F E K A L E E L A A A F P G O

TGGCTGGTTAGGTTCCGGCCGCGGACAAATACGCCGCAAAAAACCGCAACCACGTGAATTTTTTCCAGGAACGGCAGACCTCGATCGTCAG  
ACCGACCAATCCAAGCCGCGCCTGTTTATGCGGCCGTTTTTGGCGTTGGTGCACCTAAAAAAGGTCTTGACCGTCTGGAGCTAGCAGTC

273

hTCC1

G W L G S A A D K Y A G K N R N H V N F F Q E L A D L O R O

CTCATCAGCCTGATCCACGACCAGGCCAACGCGTCCAGACGACCCGCGACAAGCTTATCCTGGAGGGGCGCAAGAAAGGTCTCGAGTTCC  
GAGTAGTCGGACTAGGTGCTGGTCCGGTTGCGCCAGGTCTGCTGGGCGCTGTTTGAATAGGACCTCCCGCGTTCTTTCCAGAGCTCAAGC

364

hTCC1

Hind3

DELETED

L I S L I H O Q A N A V Q T T R O K L I L E G A K K G L E F

TGCGCCCGGTGGCTGTGGACCTGACCTACATCCCGTCTGCGGCACGCCCTATCGCCCGCTTCCAGGCGCGCTTTTGGCGGGGCGCGAT  
ACGCGGGCCACCGACACCTGGACTGGATGTAGGGCCAGCAGCCCGTGCGGGATAGCCGGCGGAAGGTCCGCGGCAAAACGCGCCCGCGCTA

455

DELETED

V R P V A V D L T Y I P V V G H A L S A A F Q A P F C A G A M

GGCCGTAGTGGGCGGCGCGCTTGCTACTTGGTCGTGAAAACGCTGATCAACGCGACTCAACTCCTCAAATTGCTTGCCAAATTGGCGGAG  
CCGGCATCACCCGCGCGCGAACCGGATGAACCAGCACTTTTGGGACTAGTTGCGCTGAGTTGAGGAGTTTAAACGAACGTTTAAACGCGCTC

546

DELETED

A V V G G A L A Y L V V K T L I N A T Q L L K L L A K L A E

TTGGTCGCGGCCGCCATTGCGGACATCATTTCCGATGTGGCGGACATCATCAAGGCGATCCTCGGAGAAGTGTGGGAGTTTCATCACAACG  
AACCAGCGCGGCGGTAACGCTGTAGTAAAGCCTACACCGCCTGTAGTAGTTCCCGTAGGAGCCTCTTCACACCTCAAGTAGTGTTCG

637

DELETED

L V A A A I A D I I S D V A D I I K G I L G E V W E F I T N

CGAAGCTTCTCAACGGCCTGAAAGAGCTTTGGGACAAGCTCACGGGGTGGGTGACCGGACTGTTCTCTCGAGGGTGGTGAACCTGGAGTC  
GCTTCGAAGAGTTGCCGGACTTTCTCGAAACCCTGTTGAGTGCCCCACCCACTGGCCTGACAAGAGAGCTCCACACGCTTGGACCTCAG

728

Hind3

hTCC1

A K L L N G L K E L W D K L T G W V T G L F S R G W S N L E S

CTTCTTTGCGGGCGTCCCGGCTTGACCGGCGGACCGAGCGGCTTGTGCAAGTGACTGGCTTGTTCGGTGGCGCCGGTCTGTCCGCATCG  
GAAGAAACGCCCGCAGGGGCCGAACCTGGCCGCGTGGTGGCGAACAGCGTTCACTGACCGAACAAGCCACGCGCGCCAGACAGGCGTAGC

819

hTCC1

F F A G V P G L T G A T S G L S O V T G L F G A A G L S A S

FIG. 9d

Sheet 1 of 2

TCGGGCTTGCTCAGCGGATAGCCTGG CTGAGCCAGCTTGCCCGCCCTGGCCGGCATTGG GGSTCCGGTTTTGGGGGCTTGC  
AGCCCGAACCAGTCCGCCCTATCGGACCGCTCGAGTCGGTCTGAACGGGCGGGACCGGCCAACCCTGGCCAGGCCAAAACCCCGAACG 910  
hTCC1  
S G L A H A D S L A S S A S L P A L A G I G G G S G F G G L  
CGAGCCTGGCTCAGGTCCATGCCGCCCTCAACTCGGCAGGCGCTACGGCCCCGAGCTGATGGCCCGGTGGCCCGCTGCCGAGCAGGTCCG 1001  
GCTCGGACCGAGTCCAGGTACGGCGGAGTTGAGCCGTCCGCGATGCCGGGGCTCGACTACCGGGCCAGCCGGCGGACGGCTCGTCCAGCC  
hTCC1  
P S L A Q V H A A S T R Q A L R P R A D G P V G A A A E Q V G  
CGGGCAGTCGCAGCTGGTCTCCGCGCAGGGTCCCAAGGTATGGGCGGACCCGTAGGCATGGCCGGCATGCACCCCTCTTCGGGGGCGTCCG 1092  
GCCCGTCAGCGTCGACCAGAGGCGCGTCCCAAGGTTCCATACCCGCCCTGGGCATCCGTACCCGCCGTACGTGGGGAGAAGCCCCCGCAAC  
hTCC1  
G Q S Q L V S A Q G S Q G M G G P V G M G G M H P S S G A S  
AAAGGGACGACGACGAAGAAGTACTCGGAAGGCGCGCGCGGGGCACTGAAGACGCCGAGCGCGCGCCAGTCGAAGCTGACGCGGGCGGTG 1183  
TTTCCCTGCTGCTGCTTCTTCATGAGCCTTCCGCGCCGCCCGCCGTGACTTCTGCGGCTCGCGCGCGGTGAGCTTCGACTGCGCCCGCCAC  
hTCC1  
K G T T T K K Y S E G A A A G T E D A E R A P V E A D A G G  
GGCAAAAGGTGCTGGTACGAAACGTCGTCTAACGGCGAATTC 1225  
CCGTTTTCCAGGACCATGCTTTGCAGCAGATTGCCGCTTAAG  
hTCC1 EcoRI  
G Q K V L V R N V V R R I

FIG. 9d  
Sheet 2 of 2



Monday, July 25, 1999 3:25 PM

ht(184-392)-H9-ht(1-129).mpd (1 > 2232) S1 d Sequence

Enzymes : 3 of 515 enzymes (Filtered)

Settings: Linear, Certain Sites Standard Genetic Code

71274134-37X-1911-111-111-111 Page 1

000101-298860

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CATATGCATCACCATCACCATCAGATGTGGCGGACATCATCAAGGGCATCTCTGGAGAAAGTGTGGAGTTTCATCACAACGGCTCAACGGCGTGAAG
GTATACGTAGTGGTAGTGGTAGTGTACACCGCTGTAGTAGTTCCTCGTAGGAGCCTCTTCACACCGCTCAAGTAGTGTTCGGCGAGTTGCCGGACTTTC
Met / HIS TAG hTCC1 (184-392)
H M H H H H H H D V A D I I K G I L G E V W E F I T N A L N G L K
AGCTTTGGGACAAGCTCACGGGGTGGGTGACCGGACTGTCTCTCGAGGGTGGTTCGAACCTGGAGTCTTCTTTGGCGGCGTCCCGGCTTGACCGGGCG
TCGAAACCGTGTTCGAGTGCCTCCACCGCTGACAAAGAGAGCTCCACCGAGCTTGGACCTCAGGAAGAAACCGCGCAGGGGGCGAACTGCGCGCG
hTCC1 (184-392)
E L W D K L T G W V T G L F S R G W S N L E S F F A G V P G L T G A
GACCAGCGGCTTGTGCAAGTGAAGTGGCTTGTTCGGTGGCGCGGTCTGTCCGCATCGTGGGCTTGGCTCAGCGGATAGCCTGGCGAGCTCAGCCAGC
CTGGTGGCGCAACAGCGTTCACTGACCGAACAAGCCAGCGCGCCAGACAGGCGTAGCAGCCCGAAGCGAGTGGCGCTATCGGACCGCTCGAGTCGGTGC
hTCC1 (184-392)
T S G L S O V T G L F G A A G L S A S S G L A H A O S L A S S A S
TTGCCCGCCCTGGCGGCAATTGGGGGCGGTTCGGTTCCTGGAGGCTGGCTCAGGTCCATGCCGCTCAACTCGGCAGGCGCTACGGCCCC
AACGGGCGGGACCGGCGTAACCCCGCGCCAGGCCAAAACCCCGAAGCGCTCGGACCGAGTCCAGGTACGGCGGAGTTGAGCCGTCCGCGATGCCGGGG
hTCC1 (184-392)
L P A L A G I G G G S G F G G L P S L A Q V H A A S T R Q A L R P
GAGCTGATGGCCCGGTTCGGCGCGCTGCCGAGCAGGTGGCGGGCAGTGCAGCTGGTCTCCGCGCAGGGTTCCCAAGGTATGGCGGACCGTAGGCAT
CTCGACTACCGGGCCAGCGCGGCGACGGCTGTCCAGCGCGCGTCAAGCTCGACCGAGGCGCGTCCCAAGGGTTCCATACCGCGCTGGGCATCCGTA
hTCC1 (184-392)
R A D G P V G A A A E Q V G G Q S Q L V S A Q G S Q G M G G P V G M
GGCGGCATGCACCCCTCTTCGGGGGCGTCAAAAGGGACGACGACGAAGAAGTACTCGGAAGGCGCGCGGGCGGCACTGAAGACCGCGAGCGCGGCCA
CCGCGCGTACGTGGGGAGAAGCCCCCGCAGCTTTCCCTGCTGCTGCTTCTTCATGAGCCTTCGCGCGCGCGCGGTGACTTCTGCGGCTCGCGCGCGGT
hTCC1 (184-392)
G G M H P S S G A S K G T T T K K Y S E G A A A G T E D A E R A P
GTCGAAGCTGACCGGGCGGTGGGCAAAAGGTGCTGGTACGAAACGTCGTCGAATTCATGGTGGATTTTCGGGGCGTTACCACCGGAGATCAACTCCGCGA
CAGCTTCGACTGCGCGCGCCACCGTTTTCCACGACCATGCTTTGCAGCAGCTTAAGTACCACCTAAAGCCCGCAATGGTGGCCTCTAGTTGAGGCGCT
hTCC1 (184-392) EcoRI TbH9
V E A D A G G S Q K V L V R N V V E F M V D F G A L P P E I N S A
GGATGTACGCGGCGCGGTTTCGGCTCGCTGGTGGCGCGGCTCAGATGTGGGACAGCGTGGCGAGTGACCTGTTTTTCGGCGCGCTCGGCGTTTTAGTC
CCTACATGCGGCGGCGCCAAAGCGGAGCGACCAACCGCGCGAGTCTACACCGTGTGCAACCGTCACTGGACAAAAGCGGCGCAGCGCAAAGTCAG
TbH9
R M Y A G P G S A S L V A A A Q M W D S V A S O L F S A A S A F Q S
GGTGGTCTGGGGTCTGACGGTGGGGTGGTGGATAGGTTCTGTCGGCGGGTCTGATGGTGGCGGCGCTCGCGGTATGTGGCGTGGATGAGCGTCACCGCG
CCACCAGACCCAGACTGCCACCCAGCACCTATCCAAGCAGCCGCCAGACTACCACCGCGCGGAGCGGCATACACCGACCTACTCGCAGTGGCGC
TbH9
V V W G L T V G S W I G S S A G L M V A A A S P Y V A W M S V T A
```

FIG. 10

Sheet 1 of 3

Sheet 2 of 3

GGATTGGAATACCCAACCAAGGGGGTATCTT CTTCACTAGAGTACTTCGAAAAAGCCCTGGAGGAGCT GCAGCGTTTCGGGGTGATGGCTG  
CCTAACCTTATGGGTTGGTTCCCCCATAGGAAATGAGGAGTGATCTCATGAAGCTTTTTCGGGACCTCTCGACCGTCTGCGCAAGGCCCACTACCGAC 2000  
hTCC1 (1-129)  
G I G I P N Q G G I L Y S S L E Y F E K A L E E L A A A F P G D G W  
GTTAGGTTGGGCGCGGACAAATACGCCGGCAAAAACCGCAACCACGTGAATTTTTTCCAGGAACCTGGCAGACCTCGATCGTCAGCTCATCAGCCTGATC 2100  
CAATCCAAGCCGGCGCCTGTTTATGCGGCGGTTTTTGGCGTTGGTGCACCTTAAAAAAGGTCTTGACCGTCTGGAGCTAGCAGTCGAGTAGTCGGACTAG  
hTCC1 (1-129)  
L G S A A D K Y A G K N R N H V N F F Q E L A D L O R O L I S L I  
CACGACCAGGCCAACGCCGTCCAGACGACCCGCGACATCCTGGAGGGCGCCAAGAAAGGTCTCGAGTTCTGCGCCCGGTGGCTGTGGACCTGACCTACA 2200  
GTGCTGGTCCGGTTGCGCCAGGTCTGCTGGGCGCTGTAGGACCTCCCGCGGTTCTTTCCAGAGCTCAAGCACGCGGGCCACCGACACCTGGACTGGATGT  
hTCC1 (1-129)  
H O O A N A V O T T R O I L E G A K K G L E F V R P V A V O L T Y  
TCCCGGTCTGTCGGGCACGCCCTATAAGATATC 2232  
AGGGCCAGCAGCCCGTGCGGGATATTCTATAG  
hTCC1 (1-129) RV  
I P V V G H A L . O I

FIG. 10

Sheet 3 of 3

000107-2498960

Monday, July 26, 1999 2:42 PM

ht(1-149)-H9-ht(161-392).mpd (1 > 2365) Site and Sequence

Enzymes : 3 of 515 enzymes (Filtered)

Settings : Circular, Certain S Only, Standard Genetic Code

Page 1

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GTATACGTAGTGGTAGTGGTAGTGTACTCGTCTCGCAAGTAGTAGCTAGGTTGCTAGTCACGGTAACTGCCGAACATCTCGGAAGACCCCT 91  
Met / HIS TAG HTCC1 (1-149)  
H M H H H H H H M S R A F I I O P T I S A I D G L Y D L L G  
TTGGAATACCCAACCAAGGGGGTATCCTTTACTCCTCACTAGAGTACTTCGAAAAAGCCCTGGAGGAGCTGGCAGCAGCGTTTCCGGGTGA  
AACCTTATGGGTTGGTTCCCCCATAGGAAATGAGCAGTATCTCATGAAGCTTTTTTCGGGACCTCCTCGACCGTCTGCGCAAAGGCCCACT 132  
HTCC1 (1-149)  
I G I P N Q G G I L Y S S L E Y F E K A L E E L A A A F P G O  
TGGCTGGTTAGGTTTCGGCCGCGGACAAATACGCCGGCAAAAAACCGCAACCACGTGAATTTTTTCCAGGAACGGCAGACCTCGATCGTCAG  
ACCGACCAATCCAAGCCGGCGCCTGTTTATGCGGCCGTTTTTGGCGTTGGTGCACCTAAAAAAGGTCCTTGACCGTCTGGAGCTAGCAGTC 273  
HTCC1 (1-149)  
G W L G S A A D K Y A G K N R N H V N F F Q E L A O L O R Q  
CTCATCAGCCTGATCCACGACCAGGCCAACGCGGTCCAGACGACCCGCGACATCCTGGAGGGCGCCAAGAAAGGTCTCGAGTTCTGTGCCG  
GAGTAGTCGGAAGTAGGTGCTGGTCCGGTTGCGCCAGGTCTGCTGGGCGCTGTAGGACCTCCCGCGGTTCTTTCCAGAGCTCAAGCAGCGG 364  
HTCC1 (1-149)  
L I S L I H D Q A N A V Q T T R D I L E G A K K G L E F V R  
CGGTGGCTGTGGACCTGACCTACATCCCGGTCTGCGGCACGCCCTATCGGCCGCTTCCAGGCGCGTTTTTGGCGGGCGCGATGGCCGT  
GCCACCGACACCTGGACTGGATGTAGGGCCAGCAGCCCGTGCGGGATAGCCGGCGGAAGGTCCGCGGCAAAACGCGCCCGCGCTACCGGCA 455  
HTCC1 (1-149)  
P V A V D L T Y I P V V G H A L S A A F Q A P F C A G A M A V  
AGTGGGCGGCGCGCTTAAGCTTATGGTGGATTTTCGGGCGGTTACCACCGGAGATCAACTCCGCGAGGATGTACGCCGGCCCGGGTTCCGGC  
TCACCCGCGCGCGAATTGAATACCACCTAAAGCCCCGCAATGGTGGCCTCTAGTTGAGGCGCTCTACATGCGGCGGGGCCCAAGCCGG 546  
HTCC1 (1-149) Hind3 TbH9  
V G G A L K L M V D F G A L P P E I N S A R M Y A G P G S A  
TCGCTGGTGGCCGCGGCTCAGATGTGGGACAGCGTGGCGAGTGACCTGTTTTTCGGCCGCGTCCGCGTTTTTCAGTCGGTGGTCTGGGGTCTGA 637  
AGCGACCACCGGCGCGGAGTCTACACCTGTGCGACCGCTCACTGGACAAAAGCCGGCGCAGCCGCAAGTCAGCCACCAGACCCCACT  
TbH9  
S L V A A A O M W D S V A S O L F S A A S A F Q S V V W G L  
CGGTGGGGTCTGTGGATAGGTTCTGTCGGCGGGTCTGATGGTGGCGGCGGTCTCGCCGTATGTGGCGTGGATGAGCGTCACCGCGGGGCAGGC 728  
GCCACCCAGCACCTATCCAAGCAGCCGCCAGACTACCACCGCCGCCAGAGCGGCATACACCGCACCTACTCGCAGTGGCGCCCGTCCG  
TbH9  
T V G S W I G S S A G L M V A A V S P Y V A W M S V T A G Q A  
CGAGCTGACCGCCGCCAGGTCCGGGTTGCTGCGGCGGCTACGAGACGGCGTATGGGCTGACGGTGGCCCCGCGGTGATCGCCGAGAAC 819  
GCTCGACTGGCGGCGGGTCCAGGCCAACGACGCCGCCGATGCTCTGCCGCATACCCGACTGCCACGGGGGCGGCCACTAGCGGCTCTTG  
TbH9  
E L T A A Q V R V A A A A Y E T A Y G L T V P P P V I A E N

FIG. 11

Sheet 1 of 3

CGTGCTGAACATGATGATTCTGATAGCGA...CTCTTGGGGCAAAACACCCCGGCGATCGCGGT...AGGCCGAATACGGCGAGATGT 910  
GCACGACTTGACTACTAAGACTATCGCTGGTTGGAGAACCCCGTTTTGTGGGGCCGCTAGCGCCAGTTCTCCGGCTTATGCCGCTCTACA  
TbH9  
R A E L M I L I A T N L L G Q N T P A I A V N E A E Y G E M  
GGGCCCCAAGACGCCGCCGCGATGTTTGGCTACGCCCGCGCGACGGCGACGGCGACGTTGCTGCGGTTCGAGGAGGCGCGCGGAGAT 1001  
CCCCGGTTCTGCGGGGGCGCTACAAACCGATCGCGCGCGCTGCCGCTGCCGCTGCAACGACGGCAAGCTCCTCCGCGGCCTCTA  
TbH9  
W A Q D A A A M F G Y A A A T A T A T A T L L P F E E A P E M  
GACCAGCGCGGGTGGGCTCCTCGACGAGGCCCGCGGGTCGAGGAGGCTCCGACACCGCGCGCGGAACCAAGTTGATGAACAATGTGCC 1092  
CTGGTCGCGCCACCCGAGGAGCTCGTCCGGCGCGCCAGCTCCTCCGAGGCTGTGGCGCGCCGCTTGGTCAACTACTTGTACACGG  
TbH9  
T S A G G L L E Q A A A V E E A S O T A A A N Q L M N N V P  
CAGGCGCTGCAACAGCTGGCCCCAGCCACGCGAGGCGACCCAGCCTTCTTCCAAGCTGGGTGGCCTGTGGAAGACGGTCTCGCCGCATCGGT 1183  
GTCCGCGACGTTGTGACCGGGTCGGGTGCGTCCCGTGGTGCGGAAGAAGTTTCGACCCACCGGACACCTTCTGCCAGAGCGGCGTAGCCA  
TbH9  
Q A L Q Q L A G P T Q G T T P S S K L G G L W K T V S P H R  
CGCCGATCAGCAACATGGTGTGATGGCCAACAACCATGTGATGACCAACTCGGGTGTGTGATGACCAACACCTTGAGCTCGATGTT 1274  
GCGGCTAGTCGTTGTACCACAGCTACCGTTGTTGGTGTACAGCTACTGGTTGAGCCACACAGCTACTGGTTGTGGAACCTGAGCTACAA  
TbH9  
S P I S N M V S M A N N H M S M T N S G V S M T N T L S S M L  
GAAGGGCTTTGCTCCGGCGGGCGGCCCGCCAGGCCGTGCAAACCGCGGCGCAAAACGGGGTCCGGGCGATGAGCTCGCTGGGCAGCTCGCTG 1365  
CTTCCCGAAACGAGGCGCGCGCGGGTCCGGCACGTTTGGCGCCGCGTTTTTGGCCAGGCCCGCTACTCGAGCGACCCGTCGAGCGAC  
TbH9  
K G F A P A A A A Q A V Q T A A Q N G V R A M S S L G S S L  
GGTTCTTCGGGTCTGGGCGGTGGGGTGGCCGCCAACTTGGGTGGGGCGGCTCGGTGGTTCGTTGTCGGTGCCGACGGCCTGGGCGCGG 1456  
CCAAGAAGCCCAGACCCGCCACCCACCGGCGGTTGAACCCAGCCCGCGGAGCCAGCCAAGCAACAGCCACGGCGTCCGGACCCGGCGCC  
TbH9  
G S S G L G G G V A A N L G R A A S V G S L S V P Q A W A A  
CCAACCAGGCAGTCACCCCGGCGGCGGGGCGCTGCCGCTGACCAGCCTGACCAGCGCCGCGGAAAGAGGGCCCGGGCAGATGCTGGGCGG 1547  
GGTTGGTCCGTCACTGGGGCCGCGCGCCGCGACGGCGACTGGTCCGACTGGTCGCGGCGCCTTTCTCCCGGGCCCGTCTACGACCCGCC  
TbH9  
A N Q A V T P A A R A L P L T S L T S A A E R G P G Q M L G G  
GCTGCCGGTGGGGCAGATGGGCGCCAGGGCCGGTGGTGGGCTCAGTGGTGTGCTGCGTGTTCGCGCGGACCCCTATGTGATGCCGATTCT 1638  
CGACGGCCACCCCGTCTACCCGCGGTCCCGGCCACCCCGAGTCACCACACGACGCACAAGGCGGCGCTGGGATACACTACGGCGTAAGA  
TbH9  
L P V G Q M G A R A G G G L S G V L R V P P R P Y V M P H S

Fig. 11

Sheet 2 of 3

CCGGCAGCCGGCAAGCTTACTCAACTCCATTGCTTGCCAAATTGGCGGAGTTGGTCGGGGATTGCGGACATCATTTCCGGATG  
GGCGGTGGCCGTTTGAATGAGTTGAGGAGTTTAACGAACGGTTTAACCGCTCAACCAGCGCGCGGTAACGCCGTGTAGTAAAGCCTAC 1729  
ToH9 Hind3 hTCC1 (161-392)  
P A A G K L T Q L L K L L A K L A E L V A A A I A D I I S D  
TGGCGGACATCATCAAGGGCATCCTCGGAGAAGTGTGGGAGTTTCATCACAACCGCGCTCAACGGCTGAAAGAGCTTTGGGACAAGCTCAC 1820  
ACCGCTGTAGTAGTTCCCGTAGGAGCCTTTCACACCCCTCAAGTAGTGTTCGGCGAGTTGCCGGACTTCTCGAAACCCTGTTCGAGTG  
hTCC1 (161-392)  
V A D I I K G I L G E V W E F I T N A L N G L K E L W O K L T  
GGGGTGGGTGACCGGACTGTTCTCTCGAGGGTGGTGAACCTGGAGTCTTCTTTGCGGGCGTCCCGGCTTGACCGGCGGACAGCGGGC 1911  
CCCCACCCACTGGCCTGACAAGAGAGCTCCACCAGCTTGACCTCAGGAAGAAACGCCCGCAGGGGCGGAAGTGGCCGCGCTGGTTCGGCG  
hTCC1 (161-392)  
G W V T G L F S R G W S N L E S F F A G V P G L T G A T S G  
TTGTGCAAGTGACTGGCTTGTTCGGTGCGGCCGGTCTGTCCGCATCGTCGGGCTTGGCTCAGCGGATAGCCTGGCGAGCTCAGCCAGCT 2002  
AACAGCGTTCACTGACCGAACAAGCCACGCCGCGCCAGACAGGCGTAGCAGCCCGAACCAGTGCCTATCGGACCGCTCGAGTCGGTCTGA  
hTCC1 (161-392)  
L S Q V T G L F G A A G L S A S S G L A H A O S L A S S A S  
TGCCCGCCCTGGCCGGCATTGGGGGCGGTCCGGTTTTGGGGGCTTCCGAGCCTGGCTCAGGTCCATGCCGCTCAACTCGGCAGGCGGT 2093  
ACGGGCGGGACCGGCCGTAACCCCGCCAGGCCAAAACCCCGAACGGCTCGGACCGAGTCCAGGTACGGCGGAGTTGAGCGTCCGCGA  
hTCC1 (161-392)  
L P A L A G I G G G S G F G G L P S L A Q V H A A S T R Q A L  
ACGGCCCCGAGCTGATGGCCCGGTGCGCGCCGCTGCCGAGCAGGTGCGCGGGCAGTCCGAGCTGGTCTCCGCGCAGGGTTCCCAAGGTATG 2184  
TGCCGGGGCTCGACTACCGGGCCAGCCGCGGCGACGGCTCGTCCAGCCGCCCGTCAGCGTCGACCAGAGGCGCGTCCCAAGGGTTCCATAC  
hTCC1 (161-392)  
R P R A D G P V G A A A E Q V G G Q S C L V S A Q G S Q G M  
GGCGGACCCGTAGGCATGGGCGGCATGCACCCCTCTTCGGGGGCGTGAAGGGACGACGACGAAGAAGTACTCGGAAGGCGCGGCGCGG 2275  
CCGCTGGGCATCCGTACCCGCCGTACGTGGGAGAGCCCCCGCAGCTTTCCTGCTGCTGCTTCTTCATGAGCCTTCCGCGCCGCGCC  
hTCC1 (161-392)  
G G P V G M G G M H P S S G A S K G T T T K K Y S E G A A A  
GCACTGAAGACGCGGAGCGCGGCCAGTCAAGCTGACCGGGCGGTGGGCAAAAGGTGCTGGTACGAAACGTCGTCTAACGGCGAATTC 2365  
CGTGACTTCTGCGGCTCGCGCGCGGTACGCTTCGACTGCGCCCGCCACCGTTTTCCACGACCATGCTTTGCAGCAGATTGCCGCTTAAG  
hTCC1 (161-392) EcoRI  
G T E D A E R A P V E A D A G G G Q K V L V R N V V R R I

FIG. 11

Sheet 3 of 3

Enzymes : 3 of 515 enzymes (Filtered)

Semings: Linear, Certain Sites Standard Genetic Code

CATATGCATCACCATCACCATCAGGATGTGGCGGACATCATCAAGGGCATCTCGGAGAAGTGTGGGAGTTCTATCACAACGGGCTCAACGGCTGAAAG  
GTATACGTAGTGGTAGTGGTAGTGTGTACACCGCTGTAGTAGTTCCTGAGGAGCCTCTTCACACCTCAAGTAGTGTGTCGCGAGTTGCCGGACTTTC 100  
Met / HIS TAG hTCC1 (184-392)  
H M H H H H H H D V A D I I K G I L G E V W E F I T N A L N G L K  
AGCTTTGGGACAAGCTCAGCGGGTGGGTGACCGGACTGTTCTCTCGAGGGTGGTGAACCTGGAGTCCTTCTTTGCGGGCTGCCCGGCTTGACCGGGCG  
TCGAAACCTGTTCGAGTGCCTCCACCCACTGGCTGACAAGAGAGCTCCACACAGCTTGGACCTCAGGAAGAAACGCCCGCAGGGGCGGAAGTGGCGCG 200  
hTCC1 (184-392)  
E L W D K L T G W V T G L F S R G W S N L E S F F A G V P G L T G A  
GACCAGCGGCTGTGCGCAAGTGAAGTGGCTTGTTCGGTGGCGGGTGTGTCCGCATCGTCGGGCTTGGCTCAGCGGATAGCCTGGCGAGCTCAGCCAGC  
CTGGTTCGCCGAACAGCGTTCACTGACCGAACAAGCCAGCGCGGCCAGACAGCGTAGCAGCCGAACCGAGTGGCGCTATCGGACCGCTCGAGTCGGTCTG 300  
hTCC1 (184-392)  
T S G L S D V T G L F G A A G L S A S S G L A H A D S L A S S A S  
TTGCCCGCCTGGCGGCAATTGGGGGCGGGTCCGGTTTTGGGGGCTTGCCGAGCCTGGCTCAGGTCCATGCCCGCTCAACTCGGCAGGCGCTACGGCCCC  
AACGGGCGGGAGCGCGCTAACCCCGCGCCAGGCCAAAACCCCGGAACGGCTCGGACCGAGTCCAGGTACGGCGGAGTTGAGCGCTCCGCGATGCCGGGG 400  
hTCC1 (184-392)  
L P A L A G I G G G S G F G G L P S L A Q V H A A S T R Q A L R P  
GAGCTGATGGCCCGGTGGCGCGGCTGCCGAGCAGGTGGCGGGCAGTTCGAGCTGGTCTCCGCGCAGGGTTCCCAAGGTATGGCGGACCCGTAGGCAT 500  
CTCGACTACCGGGCCAGCGCGGGGACGGCTCGTCCAGCGCCCGTCAGCGTCGACGAGAGGCGCGTCCCAAGGGTTCCATACCCGCTGGGCATCCGTA  
hTCC1 (184-392)  
R A D G P V G A A A E Q V G G Q S Q L V S A Q G S Q G M G G P V G M  
GGGCGGCATGCACCCCTCTTCGGGGGCGTGAAGGGGACGACGACGAAGAAGTACTCGGAAGGCGCGCGGGCGGGCACTGAAGACGCGGAGCGCGGCCA 600  
CCGCGCTACGTGGGGAGAAGCCCCCGCAGCTTTCCTGCTGCTGCTTCTTCATGAGCCTTCCGCGCGCGCGCGGTGACTTCTGCGGCTCGCGCGCGGT  
hTCC1 (184-392)  
G G M H P S S G A S K G T T T K K Y S E G A A A G T E O A E R A P  
GTGGAAGCTGACGCGGGCGGTGGGCAAAAGGTGCTGGTACGAAACGTCGTCGAATTCATGGTGGATTTCGGGGCGTTACCACCGGAGATCAACTCCGCGA 700  
CAGCTTCGACTGCGCCCCGCCACCCGTTTTCCACGACCATGCTTTGCAGCAGCTTAAGTACCACCTAAAGCCCCGCAATGGTGGCTCTAGTTGAGGCGCT  
hTCC1 (184-392) EcoRI TbH9  
V E A D A G G G Q K V L V R N V V E F M V D F G A L P P E I N S A  
GGATGTACGCGGGCGGGTTGGGCTCGCTGGTGGCGCGGCTCAGATGTGGGACAGCGTGGCGAGTGACCTGTTTTCGGCCGCGTGGCGGTTTCAGTC 800  
CCTACATGCGGCGGGGCCAAGCGGAGGACACCGGCGCGGAGTCTACACCTGTGCAACCGCTCACTGGACAAAAGCGGCGCAGCGCAAGTCAG  
TbH9  
R M Y A G P G S A S L V A A A Q M W D S V A S D L F S A A S A F Q S  
GGTGGTCTGGGGTCTGACGGTGGGGTGGTGGATAGGTTCTGTCGGCGGGTCTGATGGTGGCGGGCGCTCGCCGTATGTGGCGTGGATGAGCGTCACCGCG 900  
CCACCAGACCCAGACTGCCACCCAGCACCTATCCAAGCAGCGCCGAGACTACCACCGCGCGCGGAGCGGCATACACCGCACCTACTCGCAGTGGCGG  
TbH9  
V V W G L T V G S W I G S S A G L M V A A A S P Y V A W M S V T A

FIG. 12

Sheet 1 of 3

[illegible]

FIG. 12

Sheet 2 of 3



GGATTGGAATACCCAACCAAGGGGGTATCCTTCTCCTACTAGAGTACTTCGAAAAAGCCCTGGAGGAGCTTCAGCGTTTCCGGGTGATGGCTG  
CCTAACCTTATGGGTTGGTTCCTCCCATAGGAAATGAGGAGTGATCTCATGAAGCTTTTTCGGGACCTCCTCGACCGTCTGCGCAAGGCCCACTACCGAC  
hTCC1 (1-200)  
G I G I P N Q G G I L Y S S L E Y F E K A L E E L A A A F P G D G W  
GTTAGGTTTCGGCCGCGGACAAATACGCCGGCAAAAACCGCAACCACGTGAATTTTTTCAGGAACCTGGCAGACCTCGATCGTCAGCTCATCAGCCTGATC  
CAATCCAAGCCGGCGCCTGTTTATGCGGCCGTTTTTGGCCTTGGTGCACCTAAAAAAGGTCCTTGACCGTCTGGAGCTAGCAGTCCAGTAGTCGGACTAG  
hTCC1 (1-200)  
L G S A A D K Y A G K N R N H V N F F Q E L A D L D R O L I S L I  
CACGACCAGGCCAACCGCGTCCAGACGACCCGCGACATCTGGAGGGCGCCAAGAAAGGTCTCGAGTTCTGTGCGCCCGGTGGCTGTGGACCTGACCTACA  
GTGCTGGTCCGGTTGCGCCAGGTCTGCTGGGCGCTGTAGGACCTCCCGCGGTTCTTTCCAGAGCTCAAGCACGCGGGCCACCGACACCTGGACTGGATGT  
hTCC1 (1-200)  
H D Q A N A V Q T T R O I L E G A K K G L E F V R P V A V O L T Y  
TCCCGGTCTGTCGGGCACGCCCTATCGGCCGCCCTTCCAGGCGCGTTTTTGCGCGGGCGCGATGGCCGTAGTGGGCGGCGCGCTTGCCTACTTGGTCTGAA  
AGGGCCAGCAGCCCGTGCGGGATAGCCGGCGGAAGGTCCGCGGCAAAACGCGCCCGCGCTACCGGCATCACCGCGCGCGGAACGGATGAACCAGCACTT  
hTCC1 (1-200)  
I P V V G H A L S A A F Q A P F C A G A M A V V G G A L A Y L V V K  
AACGCTGATCAACGCGACTCAACTCCTCAAATTGCTTGCCAAATTGGCGGAGTTGGTTCGCGGCGGCCATTGCGGACATCATTTCGGATGTGCGGACATC  
TTGCGACTAGTTGCGCTGAGTTGAGGAGTTTAACGAACGGTTTAACCGCTCAACCAGCGCGCGGGTAACGCCTGTAGTAAAGCCTACACCGCCTGTAG  
hTCC1 (1-200)  
T L I N A T O L L K L L A K L A E L V A A A I A D I I S O V A D I  
ATCAAGGGCATCCTCGGAGAAGTGTTGGGAGTTCATCTAAGATATC  
TAGTTCCCGTAGGAGCCTCTTCACACCTCAAGTAGATTCTATAG  
hTCC1 (1-200) RV  
I K G I L G E V W E F I D I

FIG. 12

Sheet 3 of 3

Figure : Nucleotide sequence of MTb59

cacgactgcccgactgaacccgaactagtcagcacaacccaagtaggaagacgaaaagctatggc  
 tgagttgacaatccccgctgatgacatccagagcgcaatcgaagagtacgtaagctctttcacccg  
 cgacaccagtagagaggaagtcggtagcgtcgatgccggggacggcatcgacacgctcgaggg  
 tttgccatcgggtgatgacccaagagctgctcgaattcccgggcggaatcctcggcgtcgccctcaa  
 cctcgacgagcacagcgtcggcgcggtgatcctcgggtgacttcgagaacatcgaagaaggtcagca  
 ggtcaagcgcaccggcggaagctcttatcgggtccgggtggcgacgggtttttggggcggggtggttaa  
 cccgctcggccagccgatcgacggggcgcgagacgctcgactccgatactcggcgcgcgctggagct  
 ccaggcgccctcgggtggtgcaccggcaaggcgtgaaggagccgttgacagaccgggatcaaggcgat  
 tgacgcgatgacccccgatcggcccgggccagcgccagctgatcatcggcgaccgcaagaccggcaa  
 aaccgcccgtctgcgctcgacaccatcctcaaccagcggcagaactgggagtcgggtgatcccaagaa  
 gcagggtgcgctgtgtatcgtggccatcgggcagaagggaactaccatcgcccggttacgcccac  
 actggaagagggcggtgcatggactacaccaccatcgtcgcgggcgcgcgctcgaggtccgccc  
 tttcaaatggcttgcgccgtacaccgggttcggcgatcgcccagcactggatgtacgagggcaagca  
 tgtgctgatcatcttcgacgacctgactaagcaggccgaggcataccggggcgatctcgctgctgct  
 ggcggctccgcccggcggtgaggcctacccggcgatgtgttctatctgcattcgcggttttgga  
 gcgctgcgcccactgtccgacgatctcgggtggcggtcgctaacgggtctgccgatcatcgagac  
 caaggccaacgacatctcggcctacatcccgaccaacgctcatctcgatcaccgacgggcaatgttt  
 cctggaaaccgacctgttcaaccaggcggtccggccggccatcaacgctcgggtgtgctgggtgtcccg  
 agtcggcgggcgcgcgagatcaaggctatgaaagaggtcgccggaagcctccgcttggaaccttc  
 gcaataaccgagagctagaagctttcgccgctttcgcttctgatttggaacggcgatcgaaggcgca  
 gttggagcgcgggcgcccggtggtcgagctgctcaagcagccgcaatcccagcccatgcccgttga  
 ggagcaagtgggtttcgatcttccctgggcaccggcggtcacctggactcgggtgcccgtcgaggagct  
 ccggcggttcgaaaccgaattactggaccacatgcgggcctccgaagaagagattttgactgagat  
 ccgggacagccaaaagctcaccgaggaggccgcccgaagctcaccgaggtcatcaagaacttcaa  
 gaagggtctcgcgccaccgggtggcggtctgtgtggtgcccgaacatgtcgaggccctcgacga  
 ggataagctcgccaaggaagccgtgaagggtcaaaaagccggcgccgaagaagaagaatagctaac  
 catggctgccacacttcgcaactacgcgggcggtatcgctcggcagggtcgatcaaaaagatcac  
 caaggcccaggagctgatttgcacatcgcgcatcgccaggggcgaggctcggtcgagtcgctcg  
 gccctacgcttttgagatcaccgggatgcttaccaccctggccgctgaagccgcactggaccatcc  
 gttgct

09688672-101000

Figure . : Amino acid sequence of MTb59

MAELTI PADDI QSAIEEYVSSFTADTSREEVGTVDAGDGI AHVEGLPSVMTQELLEFPGGILGVA  
LNLDEHSVGAVILGDFENIEEGQQVKRTGEVLSVPVGDGFLGRVVPPLGQPIDGRGDVSDTRRAL  
ELQAPSVVHRQGVKEPLQTGIKAIDAMTPIGRGQRQLIIGDRKTGKTAVCVDITILNQRQNWESCDP  
KKQVRCVYVAIGQKGTIIAAVVRTLEEGGAMDYTTIVAAAASESAGFKWLAPYTGSAIAQHWMYEG  
KHVLIIFDDLTKQAEAYRAISLLLRPPGREAYPGDVFYLSRLLERCAKLSDDLGGGSLTGLPII  
ETKANDISAYIPTNVISITDGQCFLTDLFNQGV RPAINVGVSVSRVGAAQIKAMKEVAGSLRLD  
LSQYRELEAFAAFASDLDAASKAQLERGARLVELLKQPQSQPMPVEEQVVSIFLGTGGHLDSPVPE  
DVRRFETELLDHMRASEEEILTEIRDSQKLTEEAADKLTEVIKNFKKGFAATGGGSSVPDEHVEAL  
DEDKLAKEAVKVKKPAPKKKK

09688672-101000

Figure : Nucleotide sequence of MTb82

ccagcccccgccccgccccacgcccagggatgtgtggactgatggccaaagcgtcagagaccgaacgtt  
 cgggcccccgccaccaaccggcgagcggccagaccgagcgtccgagcgggttcgacccctgagca  
 cccaggcgggtgttccgccccgatctcgccgatgaggacaacttcccccatccgacgctcggccccg  
 acaccgagccgcaagaccggatggccaccaccagccgggtgcgccccgggtcagacgggtgggcg  
 gcggcctggtggaaatcccgccggcgcccgatatcgatccgcttgaggccctgatgaccaaccgg  
 tggcgccggagtcgaagcgggttctgctggaactgtggacgtcccgtcggccgggtccgactcggaga  
 ccaaggaggacttcagaggggtgggtgtccctattgcggcagcccgatattcggttcctgcgcagctaa  
 atccccggggacatcgctcgccggccagtcagaggtcaaaggctgcacgcgcacggcgagactgggct  
 ggatctacctcgctctcgaccgcaatgtcaacggccgtccgggtgggtgctcaagggcctgggtgcatt  
 ccgggtgatgccgaagcgcaggcaatggcgatggccgaacgccagttcctggccgaggtgggtgcacc  
 cgctcgatcgctgcagatcttcaactttgtcgagcacaccgacaggcacggggatccgggtcggctaca  
 tcgtgatggaatacgtcggcgggcaatcgctcaaacgcagcaagggtcagaaactgcccgctcgcg  
 agggcatcgctacctgctggagatcctgccggcgctgagctacctgcattccatcgggttgggtct  
 acaacgacctgaagccggaaaacatcatgctgaccgaggaacagctcaagctgatcgacctgggog  
 cggtatcgcggtcaactcgcttcgggtacctctacgggaccccgaggttccaggcgcccgagatcg  
 tgoggaccgggtccgacgggtggccaccgacatctacaccgtgggacgcacgctcgcgccgctcacgc  
 tggacctgcccaccgcaatggccgttatgtggatggggtacccgaagacgaccgggtgctgaaaa  
 cctacgactcttacggccgggtgctgcgcaggggccatcgaccccgatccgcggcaacgggtcacca  
 ccgcccgaagagatgtccgcgcaattgacggggcgtgttgccgggaggtgggtcgccaggacaccgggg  
 tgccgcggccagggtatcaacgatcttcagtcaccagtcgggtcgacatttgagtggtgacctgctgg  
 tggcgcacaccgacgtgtatctggacggggcaggtgcacgcgggagaagctgaccgccaacgagatcg  
 tgaccgcgctgtcggtgcccgtggtcgatccgacgcagctcgacgcttcgggtcctgcaggccacgg  
 tgctctcccagccgggtgcagaccctagactcgctgcgcgcggcccgccacgggtgcgctggacgccc  
 acggcgtcgacttctccgagtcagtgagctgcccgtaatggaagtccgcgcgctgctggatctcg  
 gcgatgtggccaaggccaccgaaaaactcgacgatctggccgaacgcgttggttggtgagtggtgat  
 tgggtctgggtaccggggcgtcgccgagctgctcacggcgactatgactcggccaccaaacatttca  
 ccgaggtgctggataacctttcccgcgagctggcgcccaagctcgccctggccgcccaccgcccgaac  
 tagccggcaacaccgacgaacacaagttctatcagacgggtgtggagcaccacgacggcggtgatct  
 cggcgggtttcgactggccagagccgggtcgcccggaaggtgatcgggtcggcgccgtgctgcacgc  
 tcgacgaggtaccgcccacttctcggtatttcaccacggcacgggtgaccagcgcggtgactctgt  
 tgtccggccgggtcaacgagtgagtcaccgaggaacagatccgcgacgcgcggccgaagagtgagg  
 cgctgcccccgaccgaaccacgcgtgctgcagatccgcgccttggtgctgggtggcgcgctggact  
 ggctgaaggacaacaaggccagcaccaaccacatcctcggtttcccggttcaccagtcacgggctgc  
 ggctgggtgtcgaggcgtcactgcgcagcctggcccggttagctcccactcaacggcatcgctaca  
 cgctgggtggacatggccaacaaggtccggccaccagcacgttctaagccgcccagtggtgaatcg

09655672-101000

Figure 1: Amino acid sequence of MTb82

MAKASETERSGPGTQPADAQTATSATVRPLSTQAVFRPDPFGDEDNFPHPPTLGPDTEPQDRMATTSR  
VRPPVRRLLGGCLVEIPRAPDIDPLEALMTNPVVPESKRFCWNCGRPVGRSDSETKGASEGWCPYCG  
SPYSFLPQLNPGLDIVAGQYEVKGCIAHGCLGWIYLAIDRNVNGRPVVLKGLVHSGDAEAQAMAMAE  
RQFLAEVWHPSIVQIFNFVEHTDRHGDPVGYIVMEYVGGQSLKRSKGQKLPVAEAIAYLLEILPAL  
SYLHSIGLVYNDLKPENIMLTTEEQLKLIDLGAVSRINSFGYLYGTPGFQAPEIVRTGPTVATDIYT  
VGRTLAALTLDLPTNRNGRYVDGLPEDDPVLKTYDSYGRLLRRAIDPDPRQRFTTAEEMSAQLTGVL  
REVVAQDTGVPRPGLSTIFSPSRSTFCVDLLVAHTDVYLDGQVHAEKLTANEIVTALSVPPLVDPTD  
VAASVLQATVLSQPVQTLDSLRAARHGALDADGVDFSESVELPLMEVRALLDLGDVAKATRKLDL  
AERVGWRWRLVWYRAVAELLTG DYDSATKHFTEVLDTFPGELAPKLALAATAELAGNTDEHKFYQT  
VWSTNDGVISAAFGGLARARSAEGDRVGAVRTLDEVPPTSRHFTTARLTSAVTLLSGRSTSEVTEEQ  
IRDAARRVEALPPTPEPRVLQIRALVLGGALDWLKD NKASTNHILGFPFTSHGLRLGVEASLRSLAR  
VAPTQRHRYTLVDMANKVRPTSTF.

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Figure 17 Amino Acid Sequence of secreted DPPD

DPPDPHQPDMTKGYCPGGRWGFGLAVCDGEKYPDGSFWHQWMQTWFTGPPQFYFDCVSGGEPLP  
GPPPPGGCGGAIPTSEQPNAP

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